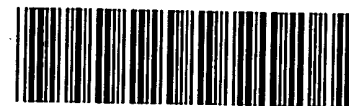


0590
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/050,763

DATE: 05/03/2002

TIME: 16:17:31

Input Set : A:\08919-067001.TXT

Output Set: N:\CRF3\05032002\J050763.raw

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4 <110> APPLICANT: Yu , Su-May
5 Shaw, Jei-Fu
7 <120> TITLE OF INVENTION: TRANSGENIC SEEDS EXPRESSING
8 AMYLOPULLULANASE AND USES THEREOF
11 <130> FILE REFERENCE: 08919-067001
13 <140> CURRENT APPLICATION NUMBER: 10/050,763
14 <141> CURRENT FILING DATE: 2002-01-16
16 <160> NUMBER OF SEQ ID NOS: 13
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29 20 25 30
30 Thr Asp Thr Ala Pro Ala Ile Ala Asn Val Val Gly Asp Phe Gln Ser
31 35 40 45
32 Lys Ile Gly Asp Ser Asp Trp Asn Ile Asn Ser Asp Lys Thr Val Met
33 50 55 60
34 Thr Tyr Lys Gly Asn Gly Phe Tyr Glu Phe Thr Thr Pro Val Ala Leu
35 65 70 75 80
36 Pro Ala Gly Asp Tyr Glu Tyr Lys Val Ala Leu Asn His Ser Trp Glu
37 85 90 95
38 Gly Gly Gly Val Pro Ser Gln Gly Asn Leu Ser Leu His Leu Asp Ser
39 100 105 110
40 Asp Ser Val Val Thr Phe Tyr Tyr Asn Tyr Asn Thr Ser Ser Val Thr
41 115 120 125
42 Asp Ser Thr Lys Tyr Thr Pro Ile Pro Glu Glu Lys Leu Pro Arg Ile
43 130 135 140
44 Val Gly Thr Ile Gln Ser Ala Ile Gly Ala Gly Asp Asp Trp Lys Pro
45 145 150 155 160
46 Glu Thr Ser Thr Ala Ile Met Arg Asp Tyr Lys Phe Asn Asn Val Tyr
47 165 170 175
48 Glu Tyr Thr Ala Asn Val Pro Lys Arg Tyr Tyr Glu Phe Lys Val Thr
49 180 185 190
50 Leu Gly Pro Ser Trp Asp Ile Asn Tyr Gly Leu Asn Gly Glu Gln Asn
51 195 200 205
52 Gly Pro Asn Ile Pro Leu Asn Val Ala Tyr Asp Thr Lys Ile Thr Phe
53 210 215 220
54 Tyr Tyr Asp Ser Val Ser His Asn Ile Trp Thr Asp Tyr Asn Pro Pro

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55 225                230                235                240
56 Leu Thr Gly Pro Asp Asn Asn Ile Tyr Tyr Asp Asp Leu Lys His Asp
57                245                250                255
58 Thr His Asp Pro Phe Phe Arg Phe Ala Phe Gly Ala Ile Lys Thr Gly
59                260                265                270
60 Asp Thr Val Thr Leu Arg Ile Gln Ala Lys Asn His Asp Leu Glu Ser
61                275                280                285
62 Ala Lys Ile Ser Tyr Trp Asp Asp Ile Lys Lys Thr Arg Thr Glu Val
63                290                295                300
64 Pro Met Tyr Lys Ile Gly Gln Ser Pro Asp Gly Gln Tyr Glu Tyr Trp
65 305                310                315                320
66 Glu Val Lys Leu Ser Phe Asp Tyr Pro Thr Arg Ile Trp Tyr Tyr Phe
67                325                330                335
68 Ile Leu Lys Asp Gly Thr Lys Thr Ala Tyr Tyr Gly Asp Asn Asp Glu
69                340                345                350
70 Gln Leu Gly Gly Val Gly Lys Ala Thr Asp Thr Val Asn Lys Asp Phe
71                355                360                365
72 Glu Leu Thr Val Tyr Asp Lys Asn Leu Asp Thr Pro Asp Trp Met Lys
73                370                375                380
74 Gly Ala Val Met Tyr Gln Ile Phe Pro Asp Arg Phe Tyr Asn Gly Asp
75 385                390                395                400
76 Pro Leu Asn Asp Arg Leu Lys Glu Tyr Ser Arg Gly Phe Asp Pro Val
77                405                410                415
78 Glu Tyr His Asp Asp Trp Tyr Asp Leu Pro Asp Asn Pro Asn Asp Lys
79                420                425                430
80 Asp Lys Pro Gly Tyr Thr Gly Asp Gly Ile Trp Asn Asn Asp Phe Phe
81                435                440                445
82 Gly Gly Asp Leu Gln Gly Ile Asn Asp Lys Leu Asp Tyr Leu Lys Asn
83                450                455                460
84 Leu Gly Ile Ser Val Ile Tyr Leu Asn Pro Ile Phe Gln Ser Pro Ser
85 465                470                475                480
86 Asn His Arg Tyr Asp Thr Thr Asp Tyr Thr Lys Ile Asp Glu Leu Leu
87                485                490                495
88 Gly Asp Leu Asp Thr Phe Lys Thr Leu Met Lys Glu Ala His Ala Arg
89                500                505                510
90 Gly Ile Lys Val Ile Leu Asp Gly Val Phe Asn His Thr Ser Asp Asp
91                515                520                525
92 Ser Ile Tyr Phe Asp Arg Tyr Gly Lys Tyr Leu Asp Asn Glu Leu Gly
93                530                535                540
94 Ala Tyr Gln Ala Trp Lys Gln Gly Asp Gln Ser Lys Ser Pro Tyr Gly
95 545                550                555                560
96 Asp Trp Tyr Glu Ile Lys Pro Asp Gly Thr Tyr Glu Gly Trp Trp Gly
97                565                570                575
98 Phe Asp Ser Leu Pro Val Ile Arg Gln Ile Asn Gly Ser Glu Tyr Asn
99                580                585                590
100 Val Lys Ser Trp Ala Asp Phe Ile Ile Asn Asn Pro Asn Ala Ile Ser
101                595                600                605
102 Lys Tyr Trp Leu Asn Pro Asp Gly Asp Lys Asp Ala Gly Ala Asp Gly
103                610                615                620

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104 Trp Arg Leu Asp Val Ala Asn Glu Ile Ala His Asp Phe Trp Val His
105 625                      630                      635                      640
106 Phe Arg Ala Ala Ile Asn Thr Val Lys Pro Asn Ala Pro Met Ile Ala
107                      645                      650                      655
108 Glu Leu Trp Gly Asp Ala Ser Leu Asp Leu Leu Gly Asp Ser Phe Asn
109                      660                      665                      670
110 Ser Val Met Asn Tyr Leu Phe Arg Asn Ala Val Ile Asp Phe Ile Leu
111                      675                      680                      685
112 Asp Lys Gln Phe Asp Asp Gly Asn Val Val His Asn Pro Ile Asp Ala
113                      690                      695                      700
114 Ala Lys Leu Asp Gln Arg Leu Met Ser Ile Tyr Glu Arg Tyr Pro Leu
115 705                      710                      715                      720
116 Pro Val Phe Tyr Ser Thr Met Asn Leu Leu Gly Ser His Asp Thr Met
117                      725                      730                      735
118 Arg Ile Leu Thr Val Phe Gly Tyr Asn Ser Ala Asn Glu Asn Gln Asn
119                      740                      745                      750
120 Ser Gln Glu Ala Lys Asp Leu Ala Val Lys Arg Leu Lys Leu Ala Ala
121                      755                      760                      765
122 Ile Leu Gln Met Gly Tyr Pro Gly Met Pro Ser Ile Tyr Tyr Gly Asp
123                      770                      775                      780
124 Glu Ala Gly Gln Ser Gly Gly Lys Asp Pro Asp Asn Arg Arg Thr Phe
125 785                      790                      795                      800
126 Ser Trp Gly Arg Glu Asp Lys Asp Leu Gln Asp Phe Phe Lys Lys Val
127                      805                      810                      815
128 Val Asn Ile Arg Asn Glu Asn Gln Val Leu Lys Thr Gly Asp Leu Glu
129                      820                      825                      830
130 Thr Leu Tyr Ala Asn Gly Asp Val Tyr Ala Phe Gly Arg Arg Ile Ile
131                      835                      840                      845
132 Asn Gly Lys Asp Val Phe Gly Asn Ser Tyr Pro Asp Ser Val Ala Ile
133                      850                      855                      860
134 Val Val Ile Asn Lys Gly Glu Ala Lys Ser Val Gln Ile Asp Thr Thr
135 865                      870                      875                      880
136 Lys Phe Val Arg Asp Gly Val Ala Phe Thr Asp Ala Leu Ser Gly Lys
137                      885                      890                      895
138 Thr Tyr Thr Val Arg Asp Gly Gln Ile Val Val Glu Val Val Ala Leu
139                      900                      905                      910
140 Asp Gly Ala Ile Leu Ile Ser Asp Pro Gly Gln Asn Leu Thr Ala Pro
141                      915                      920                      925
142 Gln Pro Ile Thr Asp Leu Lys Ala Val Ser Gly Asn Gly Gln Val Asp
143                      930                      935                      940
144 Leu Ser Trp Ser Ala Val Asp Arg Ala Val Ser Tyr Asn Ile Tyr Arg
145 945                      950                      955                      960
146 Ser Thr Val Lys Gly Gly Leu Tyr Glu Lys Ile Ala Ser Asn Val Thr
147                      965                      970                      975
148 Gln Ile Thr Tyr Ile Asp Thr Asp Val Thr Asn Gly Leu Lys Tyr Val
149                      980                      985                      990
150 Tyr Ser Val Thr Ala Val Asp Ser Asp Gly Asn Glu Ser Ala Leu Ser
151                      995                      1000                      1005
152 Asn Glu Val Glu Ala Tyr Pro Ala Phe Ser Ile Gly Trp Ala Gly Asn

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153      1010      1015      1020
154 Met Asn Gln Val Asp Thr His Val Ile Gly Val Asn Asn Pro Val Glu
155 1025      1030      1035      1040
156 Val Tyr Ala Glu Ile Trp Ala Glu Gly Leu Thr Asp Lys Pro Gly Gln
157      1045      1050      1055
158 Gly Glu Asn Met Ile Ala Gln Leu Gly Tyr Arg Tyr Ile Gly Asp Gly
159      1060      1065      1070
160 Gly Gln Asp Ala Thr Arg Asn Lys Val Glu Gly Val Glu Ile Asn Lys
161      1075      1080      1085
162 Asp Trp Thr Trp Val Asp Ala Arg Tyr Val Gly Asp Ser Gly Asn Asn
163      1090      1095      1100
164 Asp Lys Tyr Met Ala Lys Phe Val Pro Asp Met Val Gly Thr Trp Glu
165 1105      1110      1115      1120
166 Tyr Ile Met Arg Phe Ser Ser Asn Gln Gly Gln Asp Trp Thr Tyr Thr
167      1125      1130      1135
168 Lys Gly Pro Asp Gly Lys Thr Asp Glu Ala Lys Gln Phe Ile Val Val
169      1140      1145      1150
170 Pro Ser Asn Asp Val Glu Pro Pro Thr Ala Leu Gly Leu Gln Gln Pro
171      1155      1160      1165
172 Gly Ile Glu Ser Ser Arg Val Thr Leu Asn Trp Ser Leu Ser Thr Asp
173      1170      1175      1180
174 Asn Val Ala Ile Tyr Gly Tyr Glu Ile Tyr Lys Ser Leu Ser Glu Thr
175 1185      1190      1195      1200
176 Gly Pro Phe Val Lys Ile Ala Thr Val Ala Asp Thr Val Tyr Asn Tyr
177      1205      1210      1215
178 Val Asp Thr Asp Val Val Asn Gly Lys Val Tyr Tyr Tyr Lys Val Val
179      1220      1225      1230
180 Ala Val Asp Thr Ser Phe Asn Arg Thr Ala Ser Asn Ile Val Lys Ala
181      1235      1240      1245
182 Thr Pro Asp Ile Ile Pro Ile Lys Val Ile Phe Asn Val Thr Val Pro
183      1250      1255      1260
184 Asp Tyr Thr Pro Asp Asp Gly Ala Asn Ile Ala Gly Asn Phe His Asp
185 1265      1270      1275      1280
186 Ala Phe Trp Asn Pro Ser Ala His Gln Met Thr Lys Thr Gly Pro Asn
187      1285      1290      1295
188 Thr Tyr Ser Ile Thr Leu Thr Leu Asn Glu Gly Thr Gln Leu Glu Tyr
189      1300      1305      1310
190 Lys Tyr Ala Arg Gly Ser Trp Asp Lys Val Glu Lys Gly Glu Tyr Gly
191      1315      1320      1325
192 Glu Glu Ile Ala Asn Arg Lys Ile Thr Val Val Asn Gln Gly Ser Asn
193      1330      1335      1340
194 Thr Met Val Val Asn Asp Thr Val Gln Arg Trp Arg Asp Leu Pro Ile
195 1345      1350      1355      1360
196 Tyr Ile Tyr Ser Pro Lys Asp Asn Thr Thr Val Asp Ala Asn Thr Asn
197      1365      1370      1375
198 Glu Ile Glu Ile Lys Gly Asn Thr Tyr Lys Gly Ala Lys Val Thr Ile
199      1380      1385      1390
200 Asn Asp Glu Ser Phe Val Gln Gln Glu Asn Gly Val Phe Thr Lys Val
201      1395      1400      1405

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202 Val Pro Leu Glu Tyr Gly Val Asn Thr Thr Lys Ile His Val Glu Pro
203      1410                      1415                      1420
204 Ser Gly Asp Lys Asn Asn Glu Leu Thr Lys Asp Ile Thr Ile Thr Val
205 1425                      1430                      1435                      1440
206 Ile Arg Glu Glu Pro Val Gln Glu Lys Glu Pro Thr Pro Thr Pro Glu
207                      1445                      1450                      1455
208 Ser Glu Pro Ala Pro Met Pro Glu Pro Gln Pro Thr Pro Thr Pro Glu
209                      1460                      1465                      1470
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211      1475                      1480
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215 <212> TYPE: DNA
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221 gtactataca atcagcaata ggagcaggtg atgattggaa acctgaaaca tcgacagcta      180
222 taatgagaga ctataagttt aacaatgttt acgaatacac tgcaaatggt ccaaaaaggt      240
223 attatgagtt taaagtaact ttagggccct catgggatat aaattatggc ttaaattggt      300
224 aacaaaatgg tccaaatatt cctttgaatg tagcctatga tactaagatt acattttact      360
225 atgattcggg ttacataaat atatggacag attacaatcc acctctcaca gggcctgata      420
226 ataacatata ttatgacgat ttaaaacatg acacccatga ccattcttc cgcttcgctt      480
227 tcggtgcaat aaaaacaggt gatacagtga ctttgaggat acaggctaaa aatcatgacc      540
228 ttgagtcagc taaaatttct tattgggatg atattaaaaa aacaagaaca gaagtcgccg      600
229 tgtataaaat tgggtcaaagt cctgacgggc aatatgaata ctgggaagtg aagttaagct      660
230 ttgactatcc cacaagaatt tgggtattact ttatacttaa agacgggaca aaaactgctt      720
231 attacggaga taacgatgaa caattaggtg gagtaggtaa agccacagat acggtaaata      780
232 aagactttga acttactgta tacgataaaa atttagacac ccttgattgg atgaaagggg      840
233 cagtaatgta tcaaattatc ccagatagat tttacaatgg tgacccttta aatgaccgcc      900
234 taaaggaata cagtagaggt tttgatcctg ttgaatatca tgacgactgg tatgaccttc      960
235 ccgacaatcc gaatgataaa gataaacctg gatatacagg ggatggtata tggaaataatg      1020
236 acttctttgg tgggtattta caagggtata atgataaatt ggattatcta aaaaaccttg      1080
237 gaatatcagt tatttatctc aatccaattt tccaatcacc ttccaatcac cgatatgata      1140
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240 gtgatgatag tatttatTTT gatagatacg ggaagtactt ggataatgaa ttaggtgctt      1320
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249 aacttgacca aaggcttatg agcatatatg agagatatcc tcttcagta ttttattcta      1860
250 ctatgaacct ttaggtttct catgacacca tgagaatatt gacagtattt ggatataact      1920
251 ctgctaatag aaatcaaaat tctcaagagg cgaaagacct tgcagttaag aggcttaaac      1980
252 ttgccgcaat attgcaaatt ggctatccgg gaatgccttc tatttactat ggtgacgagg      2040

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VERIFICATION SUMMARY

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